

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 5.15152 Seconds
(without alignments)
91.287 Million cell updates/sec

Title: US-09-743-225-7
Perfect score: 55
Sequence: 1 CATLRVYKGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	65.5	367	1 INX4_DROME	Q9vrx6 drosophila
2	35	63.6	244	1 PHOS_MOUSE	Q9qW08 mus musculus
3	35	63.6	245	1 PHOS_BOVIN	P19632 bos taurus
4	35	63.6	245	1 PHOS_FELCA	P41686 felis silve
5	35	63.6	246	1 PHOS_RAT	P20942 rattus norv
6	35	63.6	340	1 CFAA_BACUT	Q45729 bacillus th
7	35	63.6	424	1 VGLI_HSVB	P18553 equine herp
8	35	63.6	712	1 CDGT_BACS3	P09121 bacillus sp
9	35	63.6	713	1 AMYR_BACS8	P17692 bacillus sp
10	35	63.6	713	1 CDGT_BACS0	P05618 bacillus sp
11	35	63.6	713	1 CDGT_BACSP	P30921 bacillus sp
12	35	63.6	713	1 CDGU_BACCI	P43379 bacillus ci
13	34	61.8	245	1 PHOS_CANFA	O77560 canis fami
14	34	61.8	246	1 PHOS_HUMAN	P20941 homo sapien
15	34	61.8	345	1 APOH_HUMAN	P02749 homo sapien
16	34	61.8	349	1 ADHL_ASPFL	P41747 aspergillus
17	34	61.8	349	1 ADHL_EMENI	P08843 emerice
18	34	61.8	349	1 RADA_PYRFU	O74036 pyrococcus
19	34	61.8	352	1 ADHL_EMENI	P07754 emerice
20	34	61.8	353	1 ADHL_NEUCR	Q9p6c8 neurice
21	34	61.8	356	1 RADA_PYRAB	Q9v233 pyrococcus
22	34	61.8	529	1 RADA_PYRHO	O58001 pyrococcus
23	34	61.8	633	1 DXS_BACSU	P34523 bacillus su
24	33	60.0	107	1 THIO_STRCL	Q05739 streptomyce
25	33	60.0	110	1 THIO_STRCL	P52230 streptomyce
26	33	60.0	340	1 ADHA_RHWE	Q31186 rhizobium m
27	33	60.0	483	1 CORT_DROME	Q960n3 drosophila
28	33	60.0	539	1 DOP2_DROME	Q24563 drosophila
29	33	60.0	638	1 OARI_LYMST	O77408 lymnaea sta
30	33	60.0	718	1 CDGT_BACCI	P30920 bacillus ci
31	33	60.0	718	1 CDGT_BACLI	P14014 bacillus li
32	33	60.0	718	1 CDGT_BACSS	P31747 bacillus sp
33	33	60.0	849	1 RSG2_HUMAN	Q15283 homo sapien

34	33	60.0	931	1 LUG_ARATH	Q9fuy2 arabidopsis
35	33	60.0	1111	1 MYSE_DICDI	P34092 dictyostell
36	33	60.0	1240	1 DPOL_HSV21	P07318 herpes simp
37	33	60.0	1435	1 TRB5_HUMAN	Q9y215 homo sapien
38	33	60.0	1992	1 TRIB_HUMAN	Q14669 homo sapien
39	32	58.2	298	1 PANE_BACSU	O34661 bacillus su
40	32	58.2	346	1 ANXI_RABIT	P51662 oryctolagus
41	32	58.2	351	1 ARGC_PYRAE	Q8zuu0 pyrobaculum
42	32	58.2	419	1 XHAP_BACSU	O07523 bacillus su
43	32	58.2	431	1 URTE_DESRO	P98121 desmodus ro
44	32	58.2	469	1 C1SY_FRAAN	P83372 fragaria an
45	32	58.2	477	1 URT2_DESRO	P15638 desmodus ro

ALIGNMENTS

RESULT 1
INX4_DROME STANDARD; PRT; 367 AA.
AC Q9VRX6; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 40, Last annotation update)
DE Innexin Inx4 (Innexin-4) (Zero population growth protein).
GN ZPG OR INX4 OR CG10125.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN RP
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE-Ovary;
RX MEDLINE=21959302; PubMed=11960713;
RA Stebbings L.A., Todman M.G., Phillips R., Greer C.E., Tam J.,
RA Phelan P., Jacobs K., Bacon J.P., Davies J.A.;
RT "Gap junctions in Drosophila: developmental expression of the entire
RT Innexin gene family";
RL Mech. Dev. 113:197-205(2002).
[2]
RN RP
SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE-Ovary;
RX PubMed=11973283;
RA Tazuke S.I., Schulz C., Gilboa L., Fogarty M., Mahowald A.P.,
RA Guichet A., Ephrussi A., Wood C.G., Lehmann R., Fuller M.T.;
RT "A germline-specific gap junction protein required for survival of
RT differentiating early germ cells";
RL Development 129:2529-2539(2002).
[3]
RN RP
SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20136006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Boutchan M.R., Bouck J., Brooksstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegvam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RA Science 287:2185-2195(2000).
RA [4]
RA SEQUENCE FROM N.A.
RC STRAIN-Berkeley; TISSUE-Embryo;
RX MEDLINE-22426066; PubMed-12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celnik S.E.;
RA "A *Drosophila* full-length cDNA resource.";
RA Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -1- FUNCTION: Structural component of the gap junctions in germ line
CC cells. Required for differentiation and survival of germline cysts
CC in females and of spermatogonia in males; gap junctional
CC communication between spermatogonia and somatic cyst cells may be
CC required for normal differentiation and survival of spermatogonia.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein; concentrated at
CC the interface between germline and somatic support cells in
CC spermatogonia, early spermatocytes and germ cells in the ovary.
CC -1- TISSUE SPECIFICITY: Expressed in nurse cells and oocyte during
CC oogenesis. Uniform expression in imaginal wing disk and low
CC expression in developing imaginal CNS. Expressed in embryonic pole
CC cells and primordial germ cells.
CC -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC First seen at the embryonic syncytial blastoderm stage.
CC -1- SIMILARITY: Belongs to the innexin family.
CC -----
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CC -----
DR EMBL; AF217178; AAL36976.1; -
DR EMBL; AE003562; AAF30635.1; -
DR EMBL; AY094856; AAM11209.1; -
DR FlyBase; FBgn0024177; zpg.
DR GO; GO:0007281; P:germ-cell development; IMP.
DR InterPro; IPR000990; Innexin.
DR Pfam; PF00876; Innexin; 1.
DR PRINTS; PR01262; INNEXIN.
DR KW Gap junction; Transmembrane.
FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 22 42 POTENTIAL.
FT DOMAIN 43 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 131 POTENTIAL.
FT DOMAIN 132 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 207 POTENTIAL.
FT DOMAIN 208 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 289 POTENTIAL.
FT DOMAIN 290 367 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 367 AA; 42784 MW; B984A4035DAVCF3E CRC64;
Query Match 65.5%; Score 36; DB 1; Length 367;

Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CATLRVYKGG 10
DB 237 CARCEMYKGG 246
||| :||||
||| :||||
RESULT 2
PHOS_MOUSE STANDARD; PRT; 244 AA.
ID AC Q9QW08;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosducin (PHD) (33 kDa phototransducing protein) (Rod photoreceptor
DE 1) (RPR-1).
GN PDC OR RPR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE-Retina;
RX MEDLINE-94009395; PubMed-8405193;
RA Grosman K.R., Norton J.C., Craft C.M., Travis G.H.;
RA "Isolation and characterization of a cDNA for mouse retinal
RA phosducin.";
RA Proc. Natl. Acad. Sci. USA 90:1193-1197(1993).
RL Exp. Eye Res. 57:253-255(1993).
CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC METABOLISM.
CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC the GTP-binding protein, transducin.
CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
CC -----
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CC -----
DR EMBL; L08075; AAK13559.1; -
DR PIR; JC2018; JC2018.
DR HSP; P20942; LB9X.
DR MCD; MGI:98090; Pdc.
DR InterPro; IPR001200; Phosducin.
DR InterPro; IPR008663; Thioresox_dom2.
DR Pfam; PF02114; Phosducin; 1.
DR PRINTS; PR00677; PHOSDUCIN.
DR Vision; Sensory transduction; PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 71 71
SQ SEQUENCE 244 AA; 28016 MW; F42361EA25F0F254 CRC64;
Query Match 63.6%; Score 35; DB 1; Length 244;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TLRVYKGG 10
DB 186 TLLVYKGG 193
||| :||||
||| :||||
RESULT 3
PHOS_BOVIN STANDARD; PRT; 245 AA.
ID AC P19632; P20940; Q28160;
AC P19632; P20940; Q28160;

DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).
 GN PDC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Eutheria; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE, AND SEQUENCE OF 228-245 FROM N.A.
 RC TISSUE-Retina;
 RX MEDLINE=9036806; PubMed=2203790;
 RA Lee R.H., Fowler A., McGinnis J.F., Lolley R.N., Craft C.M.;
 RT "Amino acid and cDNA sequence of bovine phosducin, a soluble
 RT phosphoprotein from photoreceptor cells.";
 RL J. Biol. Chem. 265:15867-15873(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89364083; PubMed=2770450;
 RA Kuo C.-H., Akiyama M., Miki N.;
 RT "Isolation of a novel retina-specific clone (MEKA cDNA) encoding a
 RT photoreceptor soluble protein.";
 RL Brain Res. Mol. Brain Res. 6:1-10(1989).
 RN [3]
 RP SEQUENCE OF 8-245 FROM N.A.
 RC TISSUE-Pancreas gland, and Retina;
 RX MEDLINE=91007277; PubMed=2210381;
 RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
 RA Shinohara T.;
 RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
 RT retina and pineal gland.";
 RL Gene 91:209-215(1990).
 RN [4]
 RP PHOSPHORYLATION OF SER-73.
 RX MEDLINE=9036805; PubMed=2394752;
 RA Lee R.H., Brown B.M., Lolley R.N.;
 RT "Protein kinase A phosphorylates retinal phosducin on serine 73 in
 RT situ.";
 RL J. Biol. Chem. 265:15860-15866(1990).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G-BETA AND
 G-GAMMA.
 RX MEDLINE=98416696; PubMed=9739091;
 RA Loew A., Ho Y.K., Blundell T., Bax B.;
 RT "Phosducin induces a structural change in transducin beta gamma.";
 RL Structure 6:1007-1019(1998).
 CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 CC METABOLISM.
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
 CC the GTP-binding protein, transducin.
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
 CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
 CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
 CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
 CC DUE TO A FRAMESHIFT.
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 CC
 CC EMBL; M58170; AAA62716.1;
 CC DR EMBL; M33529; AAA30349.1;
 CC DR PIR; A38379; A38379.
 CC DR PDB; 1A0R; 16-FEB-99.
 DR InterPro; IPR001200; Phosducin.

DR InterPro; IPR006663; Thioresdox_dom2.
 DR Pfam; PF02114; Phosducin; 1.
 DR PRINTS; PR00677; PHOSDUCIN.
 KW Vision; Sensory transduction; Phosphorylation; 3D-structure.
 FT MOD_RES 73 73
 FT CONFLICT 44 44
 FT CONFLICT 238 239
 FT HELIX 21 35
 FT TURN 36 36
 FT HELIX 74 80
 FT TURN 81 82
 FT HELIX 87 105
 FT STRAND 114 116
 FT HELIX 120 128
 FT TURN 132 133
 FT STRAND 135 141
 FT TURN 143 144
 FT TURN 146 147
 FT HELIX 148 161
 FT TURN 163 164
 FT STRAND 166 171
 FT HELIX 172 175
 FT TURN 178 179
 FT TURN 183 185
 FT STRAND 188 193
 FT TURN 194 195
 FT STRAND 196 201
 FT TURN 202 203
 FT HELIX 204 207
 FT TURN 210 211
 FT HELIX 214 222
 FT TURN 223 225
 SQ SEQUENCE 245 AA; 28231 MW; 5CA621610401D550 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 245;
 Best Local Similarity 87.5%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TLRVYKGG 10
 DB 188 TLRVYKGG 195
 RESULT 4
 ID PHOS_FELCA STANDARD; PRT; 245 AA.
 AC P41686;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein).
 GN PDC.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Abysinnian; TISSUE-Retina;
 RX MEDLINE=95178554; PubMed=7873608;
 RA Gorin M.B., To A.C., Narfstrom K.;
 RT "Sequence analysis and exclusion of phosducin as the gene for the
 RT recessive retinal degeneration of the Abyssinian cat.";
 RL Biochim. Biophys. Acta 1260:323-327(1995).
 CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 CC METABOLISM.
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
 CC the GTP-binding protein, transducin.
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cry15a (Insecticidal delta-endotoxin
 DE CryXA(a)) (Crystalline entomocidal protoxin) (38 kDa crystal
 DE protein).
 GN CRY15AA OR CRYXA(A).
 OS Bacillus thuringiensis (subsp. thompsoni).
 OG Plasmid.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=44162;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92105024; PubMed=1729243;
 RA Brown K.L., Whiteley H.R.;
 RT "Molecular characterization of two novel crystal protein genes from
 RT Bacillus thuringiensis subsp. thompsoni.";
 RL J. Bacteriol. 174:549-557(1992).
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPIPHILIAL CELLS OF LEPIDOPTERAN LARVAE.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -----
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 CC -----
 CC EMBL; M76442; AAA22333.1; -
 DR PIR; B41969; B41969.
 DR InterPro: IPR005831; Aer_hem.
 KW Toxin; Sporulation; Plasmid.
 SQ SEQUENCE 340 AA; 37547 MW; BCBFA24FE9B1FA50 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 340;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATLRVYKG 9
 |||:|:|
 DB 160 ATLRVYKG 167

RESULT 7
 VGLI_HSVB STANDARD; PRT; 424 AA.
 AC P18553;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Glycoprotein I precursor.
 GN GI OR 73.
 OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1),
 OS Equine herpesvirus type 1 (strain AB1) (EHV-1), and
 OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 CX NCBI_TaxID=31520, 10328, 10330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-AB4P;
 RX MEDLINE=92295566; PubMed=1318606;
 RA Teiford E.A.R., Watson M.S., McBride K., Davison A.J.;
 RT "The DNA sequence of equine herpesvirus-1";
 RL Virology 189:304-316(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AB1;
 RX MEDLINE=91276272; PubMed=1647359;
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
 RA Bonass W.A.;

RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
 RT herpesvirus type-1 short unique region.";
 RL Gene 101:203-208(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Kentucky D;
 RX MEDLINE=91108393; PubMed=2177089;
 RA Audonnet J.-C., Winslow J., Allen G., Paoletti E.;
 RT "Equine herpesvirus type 1 unique short fragment encodes
 RT glycoproteins with homology to herpes simplex virus type 1 gp, g1 and
 RT gE.";
 RL J. Gen. Virol. 71:2969-2978(1990).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GPV,
 CC AND TO PRV GP63.
 CC -----
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 CC -----
 CC EMBL; M86564; AAA02508.1; -
 DR EMBL; M36299; AAA66547.1; -
 DR PIR; C36646; VGBEE9.
 DR InterPro: IPR002874; Herpes_g1.
 DR Pfam: PF01688; Herpes_g1; 1.
 KW Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 424 GLYCOPROTEIN I.
 FT DOMAIN 23 319 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 320 340 POTENTIAL.
 FT DOMAIN 341 424 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 424 AA; 46392 MW; EE9BEF7DAA895806 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 424;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CATLRVYKGG 10
 |||:|:|:|
 DB 351 CASRRIRSG 360

RESULT 8
 CDGT_BACS3
 ID CDGT_BACS3 STANDARD; PRT; 712 AA.
 AC P09121;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase).
 GN CGT.
 OS Bacillus sp. (strain 38-2).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1412;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
 RX MEDLINE=89036108; PubMed=2972812;
 RA Kaneko T., Hamamoto T., Horikoshi K.;
 RT "Molecular cloning and nucleotide sequence of the cyclomaltodextrin
 RT glucanotransferase gene from the alkalophilic Bacillus sp. strain no.
 RT 38-2.";

RL J. Gen. Microbiol. 134:97-105(1988).
RN [2]
RP SEQUENCE OF 1-586 FROM N.A.
RA Hamamoto T., Kaneko T., Horikoshi K.;
RT "Nucleotide sequence of the cyclomaltodextrin glucanotransferase
CGTase) gene from alkalophilic Bacillus sp. strain No. 38-2";
RL Agric. Biol. Chem. 51:2019-2022(1987).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC
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CC
DR EMBL; M19880; AAA22309.1; -;
DR EMBL; D00129; BAA00077.1; -;
DR HSSP; P05618; IPAM.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRODOM; PD001568; Aamy; 1.
DR SMART; SM00632; Aamy_C; 1.
DR SMART; SM00632; Aamy_C; 1.
DR TRANSF; Glycosyltransferase; Calcium; Signal.
FT SIGNAL 1 27
FT CHAIN 28 712 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 28 165 A1.
FT DOMAIN 166 229 B.
FT DOMAIN 230 433 A2.
FT DOMAIN 434 522 C.
FT DOMAIN 523 608 D.
FT DOMAIN 609 712 E.
FT DISULFID 70 77 BY SIMILARITY.
FT ACT_SITE 256 256 BY SIMILARITY.
FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT CONFLICT 582 586 VPGGI -> SWRHL (IN REF. 2).
SQ SEQUENCE 712 AA; 78249 MW; 4FAA8F70BEF818F9 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 712;
Best Local Similarity 60.0%; Pred. NO. 30;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATLRVYKGG 10
DB 70 CTNLRLYCGG 79

RESULT 9
ID AMYR_BACS8 STANDARD; PRT; 713 AA.

PL7692;
AC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Raw-starch-digesting amylase precursor (EC 3.2.1.1) (1,4-alpha-D-
glucan glucanohydrolase).
OS Bacillus sp. (strain B1018).
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1417;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RA MEDLINE=90147765; PubMed=1689153;
RX Ithor P., Tsukagoshi N., Uda K.;
RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
Bacillus sp. B1018 and its strong homology to the cyclodextrin
glucanotransferase genes";
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC -1- FUNCTION: THIS ENDO-TYPE ADSORBABLE AMYLASE IS CAPABLE TO
DIGEST RAW-STARCH.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC
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CC
DR EMBL; M33302; AAA22239.1; -;
DR EMBL; D90112; BAA14140.1; -;
DR PIR; S09196; S09196.
DR HSSP; P43379; ICDG.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Aamy; 1.
DR SMART; SM00632; Aamy_C; 1.
DR HYDROL; Glycosidase; Carbohydrate metabolism; Calcium; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 RAW-STARCH-DIGESTING AMYLASE.
FT ACT_SITE 256 256 BY SIMILARITY.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 713;
Best Local Similarity 60.0%; Pred. NO. 30;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATLRVYKGG 10
DB 70 CTNLRLYCGG 79

RESULT 10
ID CDGT_BACS0 STANDARD; PRT; 713 AA.
AC P05618;

DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 1011).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1410;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87308036; PubMed=2957361;
RA Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
RT of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
RT acid sequence to those of alpha-amylases.";
RL J. Bacteriol. 169:4399-4402(1987).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RP Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
RA "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
RT Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
RT resolution.";
RL Acta Crystallogr. D 52:1136-1145(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL; M17366; AAA22308.1; -
DR PIR; A26678; ALBSG1.
DR PDB; 1PAM; 11-JAN-97.
DR PDB; 1D7F; 17-MAR-00.
DR PDB; 1DED; 07-APR-00.
DR PDB; 1I75; 11-APR-01.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTOEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 28 165 A1.
FT DOMAIN 166 229 B.
FT DOMAIN 230 433 A2.
FT DOMAIN 434 522 C.
FT DOMAIN 523 609 D.

FT DOMAIN 610 713
FT DISULFID 70 77
FT ACT_SITE 256 256
FT ACT_SITE 284 284
FT ACT_SITE 355 355
FT TURN 30 31
FT TURN 33 34
FT TURN 40 41
FT STRAND 44 46
FT HELIX 49 51
FT TURN 52 52
FT HELIX 57 59
FT STRAND 63 65
FT STRAND 66 66
FT TURN 68 69
FT TURN 73 74
FT STRAND 75 76
FT HELIX 81 89
FT TURN 90 93
FT HELIX 94 96
FT TURN 97 97
FT STRAND 100 103
FT STRAND 107 109
FT STRAND 114 116
FT TURN 117 118
FT STRAND 119 121
FT TURN 124 125
FT STRAND 129 135
FT TURN 137 139
FT TURN 142 154
FT TURN 155 156
FT STRAND 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 176 177
FT TURN 182 182
FT STRAND 184 186
FT TURN 187 188
FT STRAND 189 192
FT TURN 195 195
FT TURN 198 199
FT STRAND 202 202
FT STRAND 207 207
FT HELIX 213 218
FT STRAND 220 220
FT TURN 222 223
FT STRAND 224 227
FT TURN 229 230
FT HELIX 232 247
FT TURN 248 249
FT STRAND 252 255
FT TURN 256 257
FT HELIX 258 260
FT STRAND 263 276
FT STRAND 280 283
FT TURN 289 290
FT HELIX 294 302
FT STRAND 306 308
FT HELIX 310 320
FT TURN 321 322
FT HELIX 327 340
FT TURN 342 343
FT HELIX 344 346
FT STRAND 348 349
FT TURN 354 355
FT TURN 362 363
FT HELIX 366 378
FT STRAND 382 386
FT TURN 387 388
FT HELIX 389 391
FT TURN 392 392
FT TURN 398 399
FT HELIX 400 402

E. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

FT HELIX 413 421
 FT TURN 422 423
 FT HELIX 424 427
 FT HELIX 429 433
 FT STRAND 435 441
 FT STRAND 445 452
 FT TURN 453 454
 FT STRAND 455 462
 FT STRAND 469 471
 FT STRAND 475 475
 FT STRAND 481 483
 FT TURN 486 491
 FT STRAND 496 498
 FT HELIX 500 502
 FT STRAND 503 504
 FT STRAND 507 509
 FT TURN 511 512
 FT STRAND 514 519
 FT STRAND 527 532
 FT STRAND 535 536
 FT TURN 538 539
 FT STRAND 541 547
 FT STRAND 555 558
 FT TURN 559 560
 FT STRAND 561 563
 FT HELIX 565 567
 FT STRAND 568 571
 FT STRAND 575 579
 FT STRAND 586 593
 FT TURN 595 596
 FT STRAND 599 599
 FT STRAND 603 608
 FT STRAND 613 621
 FT TURN 627 628
 FT STRAND 630 635
 FT HELIX 638 640
 FT TURN 641 643
 FT HELIX 645 647
 FT STRAND 649 649
 FT STRAND 653 653
 FT TURN 660 661
 FT STRAND 663 670
 FT TURN 671 672
 FT STRAND 674 683
 FT TURN 684 685
 FT STRAND 686 689
 FT STRAND 695 698
 FT STRAND 704 710
 SQ SEQUENCE 713 AA; 524B259526B56C52 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 713;
 Best Local Similarity 60.0%; Pred. NO. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATLRYKGG 10
 DB 70 CTNRLYCGG 79

RESULT 11

ID CDGT_BACSP STANDARD; PRT; 713 AA.
 AC P30921;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase).
 GN CGT
 OS Bacillus sp. (strain 17-1).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1409;
 RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
 RX MEDLINE=90257592; PubMed=2534600;
 RA Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.;
 RT "Construction of a chimeric series of Bacillus cyclomaltodextrin
 FT glucanotransferases and analysis of the thermal stabilities and pH
 RT optima of the enzymes";
 RL J. Gen. Microbiol. 135:3447-3457(1989).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----

DR EMBL; M28053; AAA22310.1; -
 DR HSSP; P43379; LCDG.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006048; Alpha_amy1_C.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR Pfam; PF02806; alpha-amy1ase_C; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRODOM; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 KW Transferase; Glycosyltransferase; Calcium; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713
 FT DOMAIN 28 165
 FT DOMAIN 166 229
 FT DOMAIN 230 433
 FT DOMAIN 434 522
 FT DOMAIN 523 609
 FT DOMAIN 610 713
 FT DISULFID 70 77
 FT ACT_SITE 256 256
 FT ACT_SITE 284 284
 FT ACT_SITE 355 355
 SQ SEQUENCE 713 AA; 77389 MW; D13AEF6C507FF45E CRC64;

CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.

Query Match 63.6%; Score 35; DB 1; Length 713;
 Best Local Similarity 60.0%; Pred. NO. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATLRYKGG 10
 DB 70 CTNRLYCGG 79

RESULT 12

ID CDGU_BACCI STANDARD; PRT; 713 AA.
 AC P43379;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGfase).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0
RP ANGSTROMS).
RC STRAIN=251;
RX MEDLINE=94149761; PubMed=8107143;
RA Lawson C.L., van Montfort R., Strokopytov B., Rozeboom H.J.,
RA Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L., Dijkstra B.W.;
RT "Nucleotide sequence and X-ray structure of cyclodextrin
RT glycosyltransferase from *Bacillus circulans* strain 251 in a maltose-
RT dependent crystal form.";
RL J. Mol. Biol. 236:590-600(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC STRAIN=251;
RX MEDLINE=96094317; PubMed=7493956;
RA Knegtel R.M.A., Strokopytov B., Penninga D., Faber O.G.,
RA Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
RT "Crystallographic studies of the interaction of cyclodextrin
RT glycosyltransferase from *Bacillus circulans* strain 251 with natural
RT substrates and products.";
RL J. Biol. Chem. 270:29256-29264(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=97115811; PubMed=8955113;
RA Penninga D., van der Veen B.A., Knegtel R.M., van Hijum S.A.,
RA Rozeboom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.;
RT "The raw starch binding domain of cyclodextrin glycosyltransferase
RT from *Bacillus circulans* strain 251.";
RL J. Biol. Chem. 271:32777-32784(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RC STRAIN=251;
RX MEDLINE=96264806; PubMed=8672460;
RA Strokopytov B., Knegtel R.M.A., Penninga D., Rozeboom H.J., Kalk K.H.,
RA Dijkhuizen L., Dijkstra B.W.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT maltotriose inhibitor at 2.6-A resolution. Implications for product
RT specificity.";
RL Biochemistry 35:4241-4249(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds two calcium ions.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: May consist of two protein domains: the one in the amino-
CC terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
CC the other in the C-terminal side catalyzes other activities,
CC including the reconstitution of an alpha-1,4-glucosidic linkage
CC for cyclizing the maltotrioseaccharide produced.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X78145; CAA55023.1;
CC PIR; A58800; A58800.
CC PDB; 2CXG; 14-OCT-98.
CC PDB; 1CGV; 08-MAR-95.
CC PDB; 1CGW; 27-FEB-95.
CC PDB; 1CGW; 27-FEB-95.
CC PDB; 1CGY; 07-FEB-95.
CC PDB; 1CGY; 07-FEB-95.
CC PDB; 1CXE; 15-DEC-95.

DR	PDB; 1CXF; 15-DEC-95.	DR	PDB; 1CXH; 15-DEC-95.
DR	PDB; 1CXI; 15-DEC-95.	DR	PDB; 1CXJ; 15-DEC-95.
DR	PDB; 2DIJ; 13-JAN-99.	DR	PDB; 1TCM; 21-APR-97.
DR	PDB; 1CXK; 07-FEB-00.	DR	PDB; 1CXL; 03-SEP-99.
DR	PDB; 1D3C; 22-DEC-99.	DR	PDB; 1D3D; 06-MAR-00.
DR	PDB; 1D3E; 22-NOV-00.	DR	PDB; 1E07; 22-NOV-00.
DR	PDB; 1KCK; 16-JAN-02.	DR	PDB; 1KGL; 16-JAN-02.
DR	InterPro; IPR006589; Alp_amyI_cat_sub.	DR	InterPro; IPR006048; Alpha_amyI_C.
DR	InterPro; IPR006047; Alpha_amyI_cat.	DR	InterPro; IPR002044; CBD_4.
DR	InterPro; IPR002045; Glyco_hydro_13.	DR	InterPro; IPR002909; IPT_TIG.
DR	Pfam; PF00128; alpha-amyIase; 1.	DR	Pfam; PF02806; alpha-amyIase_C; 1.
DR	Pfam; PF00686; CBM_20; 1.	DR	Pfam; PF01833; TIG; 1.
DR	PRINTS; PR00110; ALPHAAMYLASE.	DR	ProDom; PD001568; CBD_4; 1.
DR	SMART; SM00642; Amy; 1.	DR	SMART; SM00632; Amy_C; 1.
KW	Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.	KW	SIGNAL
FT	CHAIN 1 27	FT	CHAIN 28 713
FT	DOMAIN 28 165	FT	DOMAIN 28 165
FT	DOMAIN 166 229	FT	DOMAIN 166 229
FT	DOMAIN 230 433	FT	DOMAIN 230 433
FT	DOMAIN 434 522	FT	DOMAIN 434 522
FT	DOMAIN 523 609	FT	DOMAIN 523 609
FT	DOMAIN 610 713	FT	DOMAIN 610 713
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FT	ACT_SITE 284 284	FT	ACT_SITE 284 284
FT	ACT_SITE 355 355	FT	ACT_SITE 355 355
FT	TURN 30 31	FT	TURN 30 31
FT	TURN 33 34	FT	TURN 33 34
FT	TURN 36 37	FT	TURN 36 37
FT	TURN 40 41	FT	TURN 40 41
FT	STRAND 44 46	FT	STRAND 44 46
FT	HELEX 49 52	FT	HELEX 49 52
FT	HELEX 57 59	FT	HELEX 57 59
FT	HELEX 63 65	FT	HELEX 63 65
FT	STRAND 66 66	FT	STRAND 66 66
FT	TURN 68 69	FT	TURN 68 69
FT	TURN 73 74	FT	TURN 73 74
FT	STRAND 76 76	FT	STRAND 76 76
FT	HELEX 81 89	FT	HELEX 81 89
FT	TURN 90 91	FT	TURN 90 91
FT	HELEX 92 96	FT	HELEX 92 96
FT	TURN 97 97	FT	TURN 97 97
FT	STRAND 100 103	FT	STRAND 100 103
FT	STRAND 107 109	FT	STRAND 107 109
FT	STRAND 114 116	FT	STRAND 114 116
FT	TURN 117 118	FT	TURN 117 118
FT	STRAND 119 121	FT	STRAND 119 121
FT	TURN 124 125	FT	TURN 124 125
FT	STRAND 129 135	FT	STRAND 129 135
FT	TURN 137 139	FT	TURN 137 139
FT	HELEX 142 154	FT	HELEX 142 154
FT	TURN 155 156	FT	TURN 155 156
FT	STRAND 158 163	FT	STRAND 158 163
FT	TURN 165 166	FT	TURN 165 166
FT	STRAND 167 170	FT	STRAND 167 170
FT	TURN 173 174	FT	TURN 173 174
FT	TURN 176 177	FT	TURN 176 177
FT	TURN 179 182	FT	TURN 179 182
FT	STRAND 184 186	FT	STRAND 184 186

CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.

NUCLEOPHILE.

PROTON DONOR.

SUBSTRATE BINDING.

FT TURN 187
 FT STRAND 188
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Query Match 63.6%; Score 35; DB 1; Length 713;
 Best Local Similarity 60.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATLRYKGG 10
 | | | | |
 DB 70 CTNRLYCGG 79

RESULT 13

PHOS_CANFA
 ID PHOS_CANFA STANDARD; PRT; 245 AA.
 AC 077560;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein).
 GN PDC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]

RP SEQUENCE FROM N.A., AND VARIANT PD GLY-82.
 RX MEDLINE-98382516; PubMed-9714819;
 RA Zhang Q., Acland G.M., Marshall C.J., Haskell J., Ray K.,
 RA Aguirre G.D.;
 RT "Characterization of canine photoreceptor phosducin cDNA and
 RT identification of a sequence variant in dogs with photoreceptor
 RT dysplasia";
 RL Gene 215:231-239(1998).
 CC -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 CC METABOLISM.
 CC -!- SUBUNIT: Forms a complex with the beta and gamma subunits of
 CC the GTP-binding protein, transducin.
 CC -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS
 CC (BY SIMILARITY).
 CC -!- DISEASE: DEFECTS IN PDC ARE THE CAUSE OF PHOTORECEPTOR DYSPLASIA
 CC (PD); AN AUTOSOMAL RECESSIVE DISEASE OF MINIATURE SCHNAUZER DOGS
 CC CAUSING RETINAL DEGENERATION.
 CC -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF046874; AAC27249.1; -;
 DR HSSP; P20942; 1B9X.
 DR InterPro; IPR001200; Phosducin.
 DR InterPro; IPR006663; Thioresox_dom2.
 DR Pfam; PF02114; Phosducin; 1.
 DR PRINTS; PR00677; PHOSDUCIN.
 KW Vision; Sensory transduction; Phosphorylation; Disease mutation.
 FT MOD_RES 73 73 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 FT VARIANT 82 R -> G (IN PD).
 SQ SEQUENCE 245 AA; 28263 MW; CFA3779E2B7DD236 CRC64;

 Query Match 61.8%; Score 34; DB 1; Length 245;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TLRVYKGG 10
 | | | | |
 DB 188 TLLIYKGG 195

 RESULT 14
 PHOS_HUMAN
 ID PHOS_HUMAN STANDARD; PRT; 246 AA.
 AC P20941; Q14816;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).
 GN PDC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pineal gland, and Retina;
 RX MEDLINE-91007277; PubMed-2210381;
 RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
 RA Shinohara T.;
 RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
 RT retina and pineal gland";
 RL Gene 91:209-215(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90343823; PubMed-2383274;

RA Watanabe Y., Kawaaki K., Miki N., Kuo C.H.;
 RT "Isolation and analysis of the human MEKA gene encoding a retina-
 RL specific protein.";
 RL Biochem. Biophys. Res. Commun. 170:951-956(1990).
 CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 CC METABOLISM.
 CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
 CC the GTP-binding protein, transducin.
 CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
 CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
 CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
 CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
 CC -1- DATABASE: NAME-Mutations of the PDC gene;
 CC NOTE-Retina International's Scientific Newsletter;
 CC WWW-http://www.retina-international.com/sci-news/pdcmut.htm".
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M33478; AAA35486.1;
 CC EMBL: M38059; AAA36210.1;
 CC EMBL: M60720; AAA36210.1; JOINED.
 CC EMBL: M38058; AAA36210.1; JOINED.
 CC PIR: A35422; A35422.
 CC HSSP: P20942; 1B9X.
 CC Genew: HGNC:8759; PDC.
 CC MIM: 171490;
 CC GO: GO:0004859; F-phospholipase inhibitor activity; TAS.
 CC GO: GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.
 CC GO: GO:0007602; P:phototransduction; TAS.
 CC InterPro: IPR001200; Phosducin.
 CC InterPro: IPR006663; Thiodox_dom2.
 CC Pfam: PF02114; Phosducin_1.
 CC PRINTS: PR00677; PHOSDUCIN.
 CC KW Vision; Sensory transduction; Phosphorylation.
 CC FT MOD_RES 73 73 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC FT CONFLICT 140 140 I -> L (IN REF. 2).
 CC FT SEQUENCE 246 AA; 28246 MW; DF59C2C7C3308C90 CRC64;
 CC SQ
 Query Match 61.8%; Score 34; DB 1; Length 246;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TLRYVKGK 10
 DB 188 TLLIYKGG 195
 RESULT 15
 APOH_HUMAN STANDARD; PRT; 345 AA.
 ID APOH_HUMAN
 AC P02749;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
 DE (Beta(2)GPI) (Activated protein C-binding protein) (APC inhibitor).
 GN APOH OR B2GI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-91315408; PubMed-1650181;
 RX Steinkasserer A., Estaller C., Weiss E., Sim R.B., Day A.J.;

RT "Complete nucleotide and deduced amino acid sequence of human beta 2-
 RL glycoprotein I.";
 RL Biochem. J. 277:387-391(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-92008618; PubMed-1655523;
 RA Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen R.R.,
 RT Moeller K.B., Moeller N.P.H., Sottrup-Jensen L.;
 RT "Molecular cloning and mammalian expression of human beta
 RL 2-glycoprotein I cDNA.";
 RL FEBS Lett. 289:183-186(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-92084151; PubMed-1748314;
 RA Mehdi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,
 RT Peoples M.E.;
 RT "Nucleotide sequence and expression of the human gene encoding
 RL apolipoprotein H (beta 2-glycoprotein I).";
 RL Gene 108:293-298(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-92273779; PubMed-1339416;
 RX Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N.,
 RA Werner P., Arnaud P.;
 RT "Molecular cloning and sequence analysis of the cDNA encoding human
 RL apolipoprotein H (beta 2-glycoprotein I).";
 RL Int. J. Clin. Lab. Res. 21:256-263(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92135065; PubMed-1777418;
 RA Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
 RA Yasuda T., Koike T.;
 RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
 RL cDNA cloning and inter-species differences of beta 2-GPI in
 RT alternation of anticardiolipin binding.";
 RL Int. Immunol. 3:1217-1221(1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99115472; PubMed-9914524;
 RA Okkels H., Rasmussen T.E., Sanghera D.K., Kamboh M.I., Kristensen T.;
 RT "Structure of the human beta2-glycoprotein I (apolipoprotein H)
 RL gene.";
 RL Eur. J. Biochem. 259:435-440(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE-84222015; PubMed-6587378;
 RX Lozier J., Takahashi N., Putnam F.W.;

RT "Complete amino acid sequence of human plasma beta 2-glycoprotein I."; [9]
RL Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
RN
RP
RC TISSUE-Follicular fluid;
RX MEDLINE-21148139; PubMed-11250549;
RA Aleporou-Marinou V., Pappa H., Yalouris P., Patargias T.;
RT "Purification of apolipoprotein H (beta 2-glycoprotein I)-like protein
RL from human follicular fluid.";
RN Comp. Biochem. Physiol. 128B:537-542(2001).
RN [10]
RP DISULFIDE BONDS IN C-TERMINAL DOMAIN.
RX MEDLINE-93050249; PubMed-1426288;
RA Steinkasserer A., Barlow P.N., Willis A.C., Kertesz Z.,
RN Campbell I.D., Sim R.B., Norman D.G.;
RT "Activity, disulphide mapping and structural modelling of the fifth
RL domain of human beta 2-glycoprotein I.";
RN FEBS Lett. 313:193-197(1992).
RN [11]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE-97299942; PubMed-9155091;
RA Gambino R., Ruiu G., Pagano G., Cassader M.;
RT "Qualitative analysis of the carbohydrate composition of
RL apolipoprotein H.";
RN J. Protein Chem. 16:205-212(1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX TISSUE-Plasma;
RX MEDLINE-99437994; PubMed-10508150;
RA Bouma B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G.,
RN Schouten A., Simmelink M.J.A., Derksen R.H.W.M., Kroon J., Gros P.;
RT "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids
RL based on its crystal structure.";
RN EMBO J. 18:5166-5174(1999).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.87 ANGSTROMS).
RX MEDLINE-20031634; PubMed-10562535;
RA Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M.,
RN Lagner P., Prasel R.;
RT "Crystal structure of human beta2-glycoprotein I: implications for
RL phospholipid binding and the antiphospholipid syndrome.";
RN EMBO J. 18:6228-6239(1999).
RN [14]
RP VARIANT LEU-266.
RX MEDLINE-93273313; PubMed-8099061;
RA Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.;
RT "Human beta 2-glycoprotein I: molecular analysis of DNA and amino
RL acid polymorphism.";
RN Hum. Genet. 91:401-402(1993).
RN [15]
RP VARIANT ASN-107.
RX MEDLINE-97369481; PubMed-9225969;
RA Sanghera D.K., Kristensen T., Hamman R.F., Kamboh M.I.;
RT "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I)
RL protein polymorphism.";
RN Hum. Genet. 100:57-62(1997).
RN [16]
RP VARIANTS GLY-325 AND SER-335.
RX MEDLINE-97217791; PubMed-9063752;
RA Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;
RT "Identification of structural mutations in the fifth domain of
RL apolipoprotein H (beta 2-glycoprotein I) which affect phospholipid
binding.";
RN Hum. Mol. Genet. 6:311-316(1997).
CC "- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
CC "- SUBCELLULAR LOCATION: Secreted.
CC "- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC "- SIMILARITY: Contains 4 Sushi (SCR) domains.
CC -----
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CC -----
CC EMBL; X58100; CAA41113.1; -
DR EMBL; X53595; CAA37664.1; -
DR EMBL; X57847; CAA40977.1; -
DR EMBL; M52839; AAA51766.1; -
DR EMBL; S80305; AAB21330.1; -
DR EMBL; Y11493; CAA72279.1; -
DR EMBL; Y11494; CAA72279.1; JOINED.
DR EMBL; Y11495; CAA72279.1; JOINED.
DR EMBL; X53595; CAA72279.1; JOINED.
DR EMBL; Y11496; CAA72279.1; JOINED.
DR EMBL; Y11497; CAA72279.1; JOINED.
DR EMBL; Y11498; CAA72279.1; JOINED.
DR EMBL; Y17754; CAA76845.1; -
DR EMBL; BC020703; AAH20703.1; -
DR EMBL; BC026283; AAH26283.1; -
DR PIR; S17178; NBHU.
DR PDB; 1QUB; 08-OCT-99.
DR PDB; 1C12; 19-NOV-99.
DR PDB; 1G4F; 28-MAR-01.
DR PDB; 1G4G; 28-MAR-01.
DR Genew; HGNC:616; APOH.
DR MIN; 138700; -
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 4.
DR SMART; SM00032; CCP; 4.
KW Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal;
KW Polymorphism; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 345 BETA-2-GLYCOPROTEIN I.
FT DOMAIN 22 80 SUSHI 1.
Query Match 61.8%; Score 34; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ATLRVYK 8
Db 151 ATLRVYK 157
Search completed: August 28, 2003, 18:35:08
Job time : 6.15152 secs